

## SEQUENCE LISTING

&lt;110&gt; PUBLIC UNIVERSITY OF NAVARRA

&lt;120&gt; "Plant nucleotide sugar

5 pyrophosphatase/phosphodiesterase (NPPase), method of  
production, use in the manufacture of testing devices  
and in the production of transgenic plants"

&lt;130&gt;

&lt;160&gt;

&lt;210&gt; 1

&lt;211&gt; 16

&lt;212&gt; Peptide

&lt;213&gt; Hordeum vulgare cv. Scarlett

&lt;220&gt;

&lt;223&gt; N-terminal end of soluble NPPase

&lt;400&gt;

Ala Ala Val Arg Ala Ser Pro Asp Leu Leu Gly Ser Arg Gly Glu  
5 10 15

Asp

&lt;210&gt; 2

&lt;211&gt; 11

&lt;212&gt; Peptide

&lt;213&gt; Hordeum vulgare cv. Scarlett

&lt;220&gt;

&lt;223&gt; Tryptic sequence of soluble NPPase

&lt;220&gt; Variant

&lt;222&gt; 6

&lt;223&gt; / Nota = Lys

&lt;220&gt; Variant

&lt;222&gt; 9

&lt;223&gt; / Nota = Ile

<220> Variant

<222> 10

<223> / Nota = Lys

<400>

Ala Ser Tyr Pro Gly Gln Thr Ser Leu Gln Arg

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10

<210> 3

<211> 11

<212> Peptide

<213> Hordeum vulgare cv. Scarlett

<220>

<223> Tryptic sequence of soluble NPPase

<220> Variant

<222> 9

<223> / Nota = Met

<400>

His Ala Pro Ala Asp Thr Val Thr Phe Gly Arg

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10

<210> 4

<211> 5

<212> Peptide

<213> Hordeum vulgare cv. Scarlett

<220>

<223> Tryptic sequence of soluble NPPase

<400>

Ala Pro Pro Tyr Pro

5

<210> 5

<211> 8

<212> Peptide

<213> Hordeum vulgare cv. Scarlett

<220>

<223> Tryptic sequence of soluble NPPase

<400>

Ala Trp Val Thr Val Glu Phe Lys

5

<210> 6

<211> 8

<212> Peptide

<213> Hordeum vulgare cv. Scarlett

<220>

<223> Tryptic sequence of soluble NPPase

<220> Variant

<222> 1

<223> / Nota = Lys

<220> Variant

<222> 3

<223> / Nota = Ile

<220> Variant

<222> 6

<223> / Nota = Ile

<400>

Gln Ser Leu Glu Gly Leu Trp Arg

5

<210> 7

<211> 15

<212> Peptide

<213> Oryza sativa

<220>

<223> N-terminal end of soluble NPPase

<400>

Gly Ser Ala Phe Val Ser Ala Thr Pro Ala Leu Leu Gly Asp Gln

5

10

15

<210> 8

<211> 23

<212> Peptide

<213> Oryza sativa

<220>

<223> Tryptic sequence (MS/MS) of soluble NPPase

<400>

Phe Gln Leu Leu Asn Gln Arg Tyr Asp Phe Ser Phe Ala Leu Glu

5

10

15

Thr Gly Gly Leu Glu Asn Pro Lys

20

<210> 9

<211> 11

<212> Peptide

<213> Oryza sativa

<220>

<223> Tryptic sequence (MS/MS) of soluble NPPase

<400>

Leu Val Ala Val Ser Glu Ala Leu Ser Phe Lys

5

10

<210> 10

<211> 10

<212> Peptide

<213> Oryza sativa

<220>

<223> Tryptic sequence (Edman) of soluble NPPase

<400>

Leu Ala Gln Gly Lys Ser Tyr Asp Glu Met

5

10

<210> 11

<211> 10

<212> Peptide

<213> Oryza sativa

<220>

<223> Tryptic sequence (MS/MS) of soluble NPPase

<400>

Thr Ala Ala Gly Thr Leu Thr Phe Asn Arg

5

10

<210> 12

<211> 11

<212> Peptide

<213> Oryza sativa

<220>

<223> Tryptic sequence (MS/MS) of soluble NPPase

<400>

Asp Pro Gly Phe Leu His Thr Ala Phe Leu Arg  
5 10

<210> 13

<211> 12

<212> Peptide

<213> Oryza sativa

<220>

<223> Tryptic sequence (MS/MS) of soluble NPPase

<400>

Ala Pro Asp Phe Pro Gly Gln Asn Ser Leu Gln Arg  
5 10

<210> 14

<211> 9

<212> Peptide

<213> Oryza sativa

<220>

<223> Tryptic sequence (MS/MS) of soluble NPPase

<400>

Ile Ile Val Phe Gly Asp Met Gly Lys  
5

<210> 15

<211> 12

<212> Peptide

<213> Oryza sativa

<220>

<223> Tryptic sequence (MS/MS) of soluble NPPase

<400>

Asp Trp Pro Asn Thr Gly Gly Phe Phe Asp Val Lys

5

10

<210> 16

<211> 11

<212> Peptide

<213> Oryza sativa

<220>

<223> Tryptic sequence (MS/MS) of soluble NPPase

<400>

Phe Ile Glu Gln Cys Leu Ser Thr Val Asp Arg

5

10

<210> 17

<211> 9

<212> Peptide

<213> Oryza sativa

<220>

<223> Tryptic sequence (MS/MS) of soluble NPPase

<400>

Val Tyr Asp Ser Phe Tyr Val Glu Arg

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<210> 18

<211> 18

<212> ADN

<213> Oryza sativa

<220>

<223> Primer of the 5' region of NPPase

<400>

ggcgttgctc ggcgacca

<210> 19

<211> 19

<212> ADN

<213> *Oryza sativa*

<220>

<223> Primer of the 3' region of NPPase

<400>

gaggcgagcg tgggtgggga

<210> 20

<211> 2186

<212> ADN

<213> *Oryza sativa*

<220>

<223> complete cDNA of rice NPPase

<400>

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ggc	gtg	gca	atg	gcg	gtg	gcg	atg	ctg	ctg	90
gcg	gcg	gcg	agc	gcg	tcg	cgg	ccg	tcg	tcg	120
tcg	ctg	gaa	ggg	ttc	cag	ccg	ctg	tcg	aag	150
atc	gcc	gtc	cac	aag	gcc	acc	gtc	gac	ctc	180
cac	ggc	tcc	gcg	ttc	gtc	agc	gcc	acg	ccg	210
gcg	ttg	ctc	ggc	gac	cag	gga	gaa	gac	aca	240
gag	tgg	gtc	acg	gtg	aaa	tac	ggc	tgg	gca	270
aac	cct	tcc	gct	gac	gac	tgg	att	gct	gtc	300
ttc	tct	ccg	gcc	gat	ttc	atc	tcg	ggg	tct	330
tgc	cct	aat	cct	tcc	aga	tac	ccg	gat	gag	360
ccg	ctg	ctc	tgc	act	gca	cca	ata	aag	tat	390
caa	ttc	gca	aac	tac	tcg	gcg	aac	tac	gtg	420
tac	tgg	ggc	aag	ggc	agc	atc	cgg	ttc	cag	450
ctc	atc	aac	cag	cgc	tac	gac	ttc	tcc	ttc	480
gcc	ctg	ttc	acc	ggc	ggc	ctg	gaa	aac	cct	510



aag ctg gtg gcg gtg tcg gag gcg ata tcg 540  
ttc aag aac ccc aag gcg ccg gtg tac cct 570  
cgg ctg gcg cag ggc aag tcg tac gac gag 600  
atg acc gtc aca tgg acc agc ggc tac gac 630  
atc agc gag gcg tac ccg ttc gtc gag tgg 660  
ggc atg gtc gtc gcc ggc gcc gcc gct cca 690  
acc cgc acc gcc gcc ggc acg ctc acc ttc 720  
aac cgc ggc agc atg tgc ggt gac ccg gac 750  
cgc act gtt ggg tgg aga gac ccc ggg ttc 780  
atc cac aca gct ttc ctg aga gac ctg tgg 810  
ccc aac aaa gag tac tac tac aag att ggg 840  
cat gaa ctt tct gac gga tca att gtc tgg 870  
ggc aag caa tac act ttc cgg gcg cca ccc 900  
ttc cct ggc cag aac tcg ctg caa cgc atc 930  
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aga gac gga tca aac gag ttc gcc aac tac 990  
cag cca gga tct ctg aac acg acg gac agg 1020  
ctg gtc gag gat ctg gac aac tac gac att 1050  
gtc ttc cac atc ggt gat ctt ccg tac gcc 1080  
aat ggc tac atc tcc cag tgg gac cag ttc 1110  
acc gcc cag gtc gcc ccc atc acc gcc aag 1140  
aag ccc tac atg att gca agc ggt aac cat 1170  
gag agg gac tgg ccc aac acc gga ggg ttc 1200  
ttc gac gtc aag gac tcc ggc ggc gag tgc 1230  
ggc gtt ccg gca gag acc atg tac tac tac 1260  
ccg gcc gag aat cga gcc aac ttc tgg tac 1290  
aag gtg gac tac ggg atg ttc cgg ttc tgc 1320  
atc gcg gac tcg gag cac gac tgg agg gag 1350  
ggt acc gac cag tac aag ttc atc gag cag 1380  
tgc ctg tcg acg gtg gac cgg aag cac cag 1410  
ccg tgg ctc atc ttc gcg gcg cac cgc gtg 1440  
ctg ggc tac tcc tcc aac tgg tgg tac gcc 1470  
gac cag ggc tcc ttc gag gag ccc gaa ggg 1500  
agg gag agc ctg cag cgg ctg tgg cag cgc 1530  
cac cgc gtc gac gtc gcc ttc ttc ggc cac 1560  
gtc cac aac tac gag cgg acg tgc ccg atg 1590  
tac cag agc cag tgc gtc tcc ggc gag agg 1620  
cgc cgc tac tcc ggc acc atg aac ggc acc 1650  
atc ttc gtc gtc gcc ggc ggc ggc ggg agc 1680  
cac ctc tcg gac tac acc tcg gcg atc ccc 1710  
aag tgg agc gtt ttc agg gac cgg gac ttc 1740  
ggg ttc gtc aag ctc acc gcg ttc aac cac 1770  
tcg tcg ctg ctg ttc gag tac aag aag agc 1800  
agc gat ggg aag gtg tat gac tcc ttc acc 1830  
gtg gag agg gat tac cgc gac gtg ctc agc 1860  
tgc gtg cac gac agc tgc ctc ccc acc acg 1890  
ctc gcc tcc tga tga atg aaa caa ggg aaa 1920  
gga tca tta tta gga tgc atg agt tga tgc 1950

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ctc atc gtc aaa atg ctg gca gct gag aaa 1980
gag tga tcg gtc ggt cga tcg agt tgg gtt 2010
tta ttt ttt ttc ttc ttc ttc aac cat ttc 2040
gat cag gtg tgg tag tgg tcg atc gct tgg 2070
ctc gat cgt gtt tct ctt cct cat gga tgg 2100
tga tgt tgt gca ata aaa ttg ctt agc tgc 2130
tcg ggc aca aat gtc taa aaa aaa aaa 2160
aaa aaa aaa aaa aaa aaa aaa aa      2186

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<210> 21

<211> 623

<212> Peptide

<213> *Oryza sativa*

<220>

<223> Amino acid sequence of rice NPPase

<400>

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      25      30      35      40
Ile Ala Val His Lys Ala Thr Val Asp Leu His Gly Ser Ala Phe Val Ser Ala Thr Pro
      45      50      55      60
Ala Leu Leu Gly Asp Gln Gly Glu Asp Thr Glu Trp Val Thr Val Lys Tyr Gly Trp Ala
      65      70      75      80
Asn Pro Ser Ala Asp Asp Trp Ile Ala Val Phe Ser Pro Ala Asp Phe Ile Ser Gly Ser
      85      90      95      100
Cys Pro Asn Pro Ser Arg Tyr Pro Asp Glu Pro Leu Leu Cys Thr Ala Pro Ile Lys Tyr
      105      110      115      120
Gln Phe Ala Asn Tyr Ser Ala Asn Tyr Val Tyr Trp Gly Lys Gly Ser Ile Arg Phe Gln
      125      130      135      140
Leu Ile Asn Gln Arg Tyr Asp Phe Ser Phe Ala Leu Phe Thr Gly Gly Leu Glu Asn Pro
      145      150      155      160
Lys Leu Val Ala Val Ser Glu Ala Ile Ser Phe Lys Asn Pro Lys Ala Pro Val Tyr Pro
      165      170      175      180
Arg Leu Ala Gln Gly Lys Ser Tyr Asp Glu Met Thr Val Thr Trp Thr Ser Gly Tyr Asp
      185      190      195      200
Ile Ser Glu Ala Tyr Pro Phe Val Glu Trp Gly Met Val Val Ala Gly Ala Ala Ala Pro
      205      210      215      220
Thr Arg Thr Ala Ala Gly Thr Leu Thr Phe Asn Arg Gly Ser Met Cys Gly Asp Pro Asp
      225      230      235      240
Arg Thr Val Gly Trp Arg Asp Pro Gly Phe Ile His Thr Ala Phe Leu Arg Asp Leu Trp
      245      250      255      260
Pro Asn Lys Glu Tyr Tyr Tyr Lys Ile Gly His Glu Leu Ser Asp Gly Ser Ile Val Trp
      265      270      275      280
Gly Lys Gln Tyr Thr Phe Arg Ala Pro Pro Phe Pro Gly Gln Asn Ser Leu Gln Arg Ile
      285      290      295      300
Ile Val Phe Gly Asp Met Gly Lys Ala Glu Arg Asp Gly Ser Asn Glu Phe Ala Asn Tyr
      305      310      315      320
Gln Pro Gly Ser Leu Asn Thr Thr Asp Arg Leu Val Glu Asp Leu Asp Asn Tyr Asp Ile
      325      330      335      340

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Val Phe His Ile Gly Asp Leu Pro Tyr Ala Asn Gly Tyr Ile Ser Gln Trp Asp Gln Phe  
 345 350 355 360  
 Thr Ala Gln Val Ala Pro Ile Thr Ala Lys Lys Pro Tyr Met Ile Ala Ser Gly Asn His  
 365 370 375 380  
 Glu Arg Asp Trp Pro Asn Thr Gly Gly Phe Phe Asp Val Lys Asp Ser Gly Gly Glu Cys  
 385 390 395 400  
 Gly Val Pro Ala Glu Thr Met Tyr Tyr Tyr Pro Ala Glu Asn Arg Ala Asn Phe Trp Tyr  
 405 410 415 420  
 Lys Val Asp Tyr Gly Met Phe Arg Phe Cys Ile Ala Asp Ser Glu His Asp Trp Arg Glu  
 425 430 435 440  
 Gly Thr Asp Gln Tyr Lys Phe Ile Glu Gln Cys Leu Ser Thr Val Asp Arg Lys His Gln  
 445 450 455 460  
 Pro Trp Leu Ile Phe Ala Ala His Arg Val Leu Gly Tyr Ser Ser Asn Trp Trp Tyr Ala  
 465 470 475 480  
 Asp Gln Gly Ser Phe Glu Glu Pro Glu Gly Arg Glu Ser Leu Gln Arg Leu Trp Gln Arg  
 485 490 495 500  
 His Arg Val Asp Val Ala Phe Phe Gly His Val His Asn Tyr Glu Arg Thr Cys Pro Met  
 505 510 515 520  
 Tyr Gln Ser Gln Cys Val Ser Gly Glu Arg Arg Arg Tyr Ser Gly Thr Met Asn Gly Thr  
 525 530 535 540  
 Ile Phe Val Val Ala Gly Gly Gly Gly Ser His Leu Ser Asp Tyr Thr Ser Ala Ile Pro  
 545 550 555 560  
 Lys Trp Ser Val Phe Arg Asp Arg Asp Phe Gly Phe Val Lys Leu Thr Ala Phe Asn His  
 565 570 575 580  
 Ser Ser Leu Leu Phe Glu Tyr Lys Lys Ser Ser Asp Gly Lys Val Tyr Asp Ser Phe Thr  
 585 590 595 600  
 Val Glu Arg Asp Tyr Arg Asp Val Leu Ser Cys Val His Asp Ser Cys Leu Pro Thr Thr  
 605 610 615 620  
 Leu Ala Ser

<210> 22

<211> 1268

<212> ADN

<213> Hordeum vulgare cv. Scarlett

<220>

<223> incomplete cDNA of barley NPPase

<400>

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 cta cac ttt ccg ggc acc gcc aac ccc cgg 60  
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 cgg tga cat ggg aaa ggc gga gag gga cgg 120  
 atc aaa cga gtt cgc caa cta cca gcc ggg 150  
 gtc gct caa cac gac gga cag gct gat tga 180  
 aga tct gga caa cta cga cat cgt ctt cca 210  
 cat cgg cga cat gcc cta cgc caa cgg gta 240  
 cct ctc cca gtg gga cca gtt cac cgc aca 270  
 ggt cgc ccc cat cag cgc caa gaa acc cta 300  
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 ctg gcc caa cac cgg cgg gtt ctt cga cgt 360

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caa gga ctc cgg cgg cga atg cgg cgt gcc 390
ggc cga gac cat gta cta cta ccc cgc cga 420
aaa cag ggc aaa ctt ctg gta caa ggt gga 450
cta cgg gat gtt ccg gtt ctg cgt ggg gga 480
ctc gga gca cga ctg gag gga ggg cac ccc 510
gca gta caa gtt cat cga gga gtg cct gtc 540
gac ggt gga ccg gaa gca cca gcc gtg gct 570
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ctc ctc caa ctc gtg gta cgc cga cca ggg 630
ctc ctt cga gga gcc cga ggg acg gga gag 660
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cga cat cgc ctc ctt cgg cca cgt cca caa 720
cta cga gcg cac atg ccc gct cta cca gag 750
cca gtg cgt caa cgc cga caa gac cca cta 780
ctc ggg cac cat gaa cgg cac cat ctt cgt 810
cgt cgc cgg cgg ggg cgg cag cca cct gtc 840
gtc cta cac cac cgc cat ccc caa gtg gag 870
cat att cag gga cca tga cta cgg gtt cac 900
caa gct cac cgc att caa cca ctc ctc gct 930
tct ctt cga gta cat gaa gag cag cga cgg 960
caa ggt cta cga ctc ctt cac cat cca cag 990
gga tta ccg cga cgt gct cag ctg cgt gca 1020
cga cag ctg ctt ccc cac cac gct cgc tag 1050
cta gct cat atc gtc cgg ccg tca tgt caa 1080
tgt aat gga ggg tca tcc atc caa taa aat 1110
tgt ggg cat gtg ttg agt aat aaa att ggt 1140
cag ctg cac aat tta tat gtg cta gta aaa 1170
aga tca tgc aag agg tgg gtg tat gct cgt 1200
tat ata tgc ttt gta act cct tca tgt cat 1230
att att atg ggt taa taa aaa cat cct tta 1260
tta aaa aa 1268

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<210> 23

<211> 350

<212> Peptide

<213> Hordeum vulgare cv. Scarlett

<220>

<223> Amino acid sequence deduced from the cDNA of barley NPPase

&lt;400&gt;

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Gln	Asn	Ser	Leu	Gln	Arg	Ile	Ile	Val	Phe	Gly	Asp	Met	Gly	Lys	Ala	Glu	Arg	Asp	Gly	
				25					30					35					40	
Ser	Asn	Glu	Phe	Ala	Asn	Tyr	Gln	Pro	Gly	Ser	Leu	Asn	Thr	Thr	Asp	Arg	Leu	Ile	Glu	
				45					50					55					60	
Asp	Leu	Asp	Asn	Tyr	Asp	Ile	Val	Phe	His	Ile	Gly	Asp	Met	Pro	Tyr	Ala	Asn	Gly	Tyr	
				65					70					75					80	
Leu	Ser	Gln	Trp	Asp	Gln	Phe	Thr	Ala	Gln	Val	Ala	Pro	Ile	Ser	Ala	Lys	Lys	Pro	Tyr	
				85					90					95					100	
Met	Val	Ala	Ser	Gly	Asn	His	Glu	Arg	Asp	Trp	Pro	Asn	Thr	Gly	Gly	Phe	Phe	Asp	Val	
				105					110					115					120	
Lys	Asp	Ser	Gly	Gly	Glu	Cys	Gly	Val	Pro	Ala	Glu	Thr	Met	Tyr	Tyr	Tyr	Pro	Ala	Glu	
				125					130					135					140	
Asn	Arg	Ala	Asn	Phe	Trp	Tyr	Lys	Val	Asp	Tyr	Gly	Met	Phe	Arg	Phe	Cys	Val	Gly	Asp	
				145					150					155					160	
Ser	Glu	His	Asp	Trp	Arg	Glu	Gly	Thr	Pro	Gln	Tyr	Lys	Phe	Ile	Glu	Glu	Cys	Leu	Ser	
				165					170					175					180	
Thr	Val	Asp	Arg	Lys	His	Gln	Pro	Trp	Leu	Ile	Phe	Thr	Ala	His	Arg	Val	Leu	Gly	Tyr	
				185					190					195					200	
Ser	Ser	Asn	Ser	Trp	Tyr	Ala	Asp	Gln	Gly	Ser	Phe	Glu	Glu	Pro	Glu	Gly	Arg	Glu	Ser	
				205					210					215					220	
Leu	Gln	Lys	Leu	Trp	Gln	Arg	Tyr	Arg	Val	Asp	Ile	Ala	Ser	Phe	Gly	His	Val	His	Asn	
				225					230					235					240	
Tyr	Glu	Arg	Thr	Cys	Pro	Leu	Tyr	Gln	Ser	Gln	Cys	Val	Asn	Ala	Asp	Lys	Thr	His	Tyr	
				245					250					255					260	
Ser	Gly	Thr	Met	Asn	Gly	Thr	Ile	Phe	Val	Val	Ala	Gly	Gly	Gly	Gly	Ser	His	Leu	Ser	
				265					270					275					280	
Ser	Tyr	Thr	Thr	Ala	Ile	Pro	Lys	Trp	Ser	Ile	Phe	Arg	Asp	His	Asp	Tyr	Gly	Phe	Thr	
				285					290					295					300	
Lys	Leu	Thr	Ala	Phe	Asn	His	Ser	Ser	Leu	Leu	Phe	Glu	Tyr	Met	Lys	Ser	Ser	Asp	Gly	
				305					310					315					320	
Lys	Val	Tyr	Asp	Ser	Phe	Thr	Ile	His	Arg	Asp	Tyr	Arg	Asp	Val	Leu	Ser	Cys	Val	His	
				325					330					335					340	
Asp	Ser	Cys	Phe	Pro	Thr	Thr	Leu	Ala	Ser											
				345					350											

&lt;210&gt; 24

&lt;211&gt; 39

&lt;212&gt; ADN

&lt;213&gt; Hordeum vulgare cv. Scarlett

&lt;220&gt;

&lt;223&gt; Primer of the 5' region of NPPase

soluble

&lt;400&gt;

gcagcagttac gagcatcacc agatctacta gcatcacga

39